

**Figure 1**

**Cell-Based cAMP Assay**

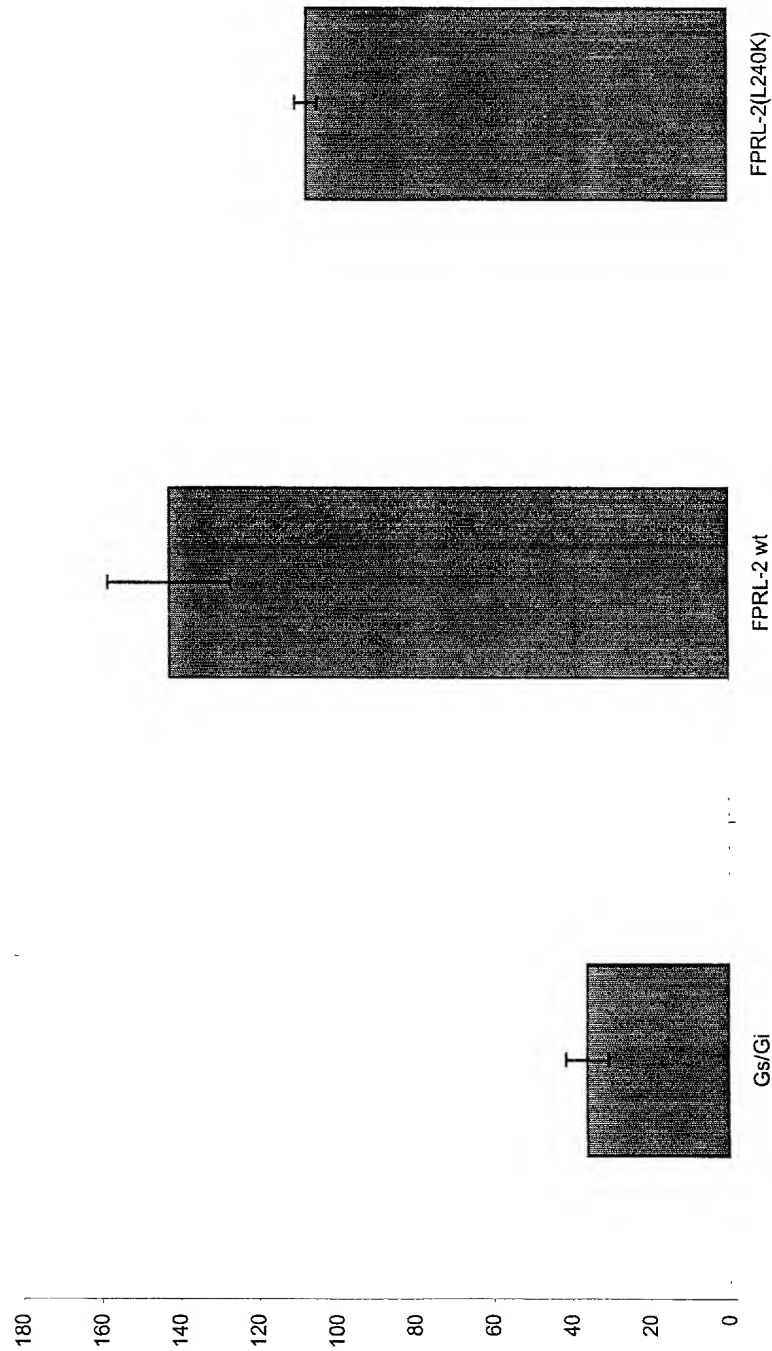
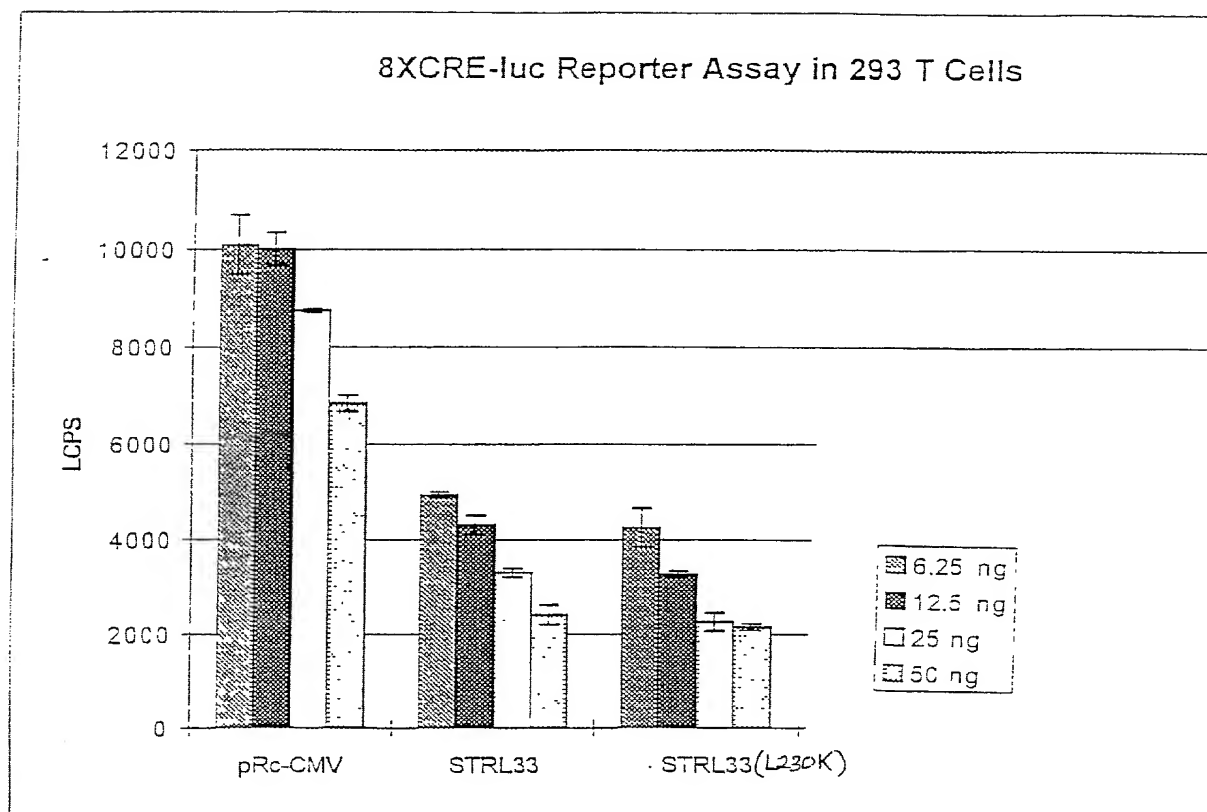


Figure 2



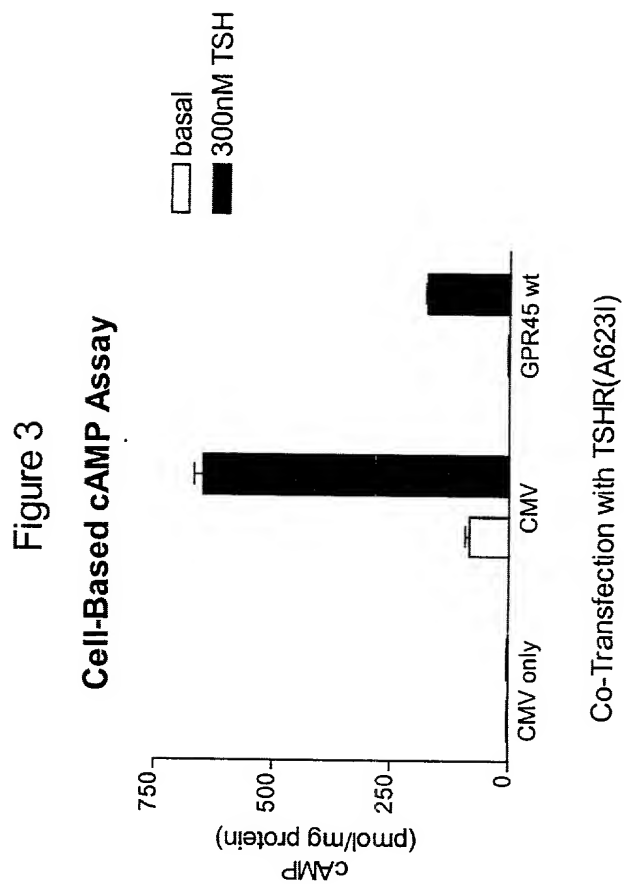
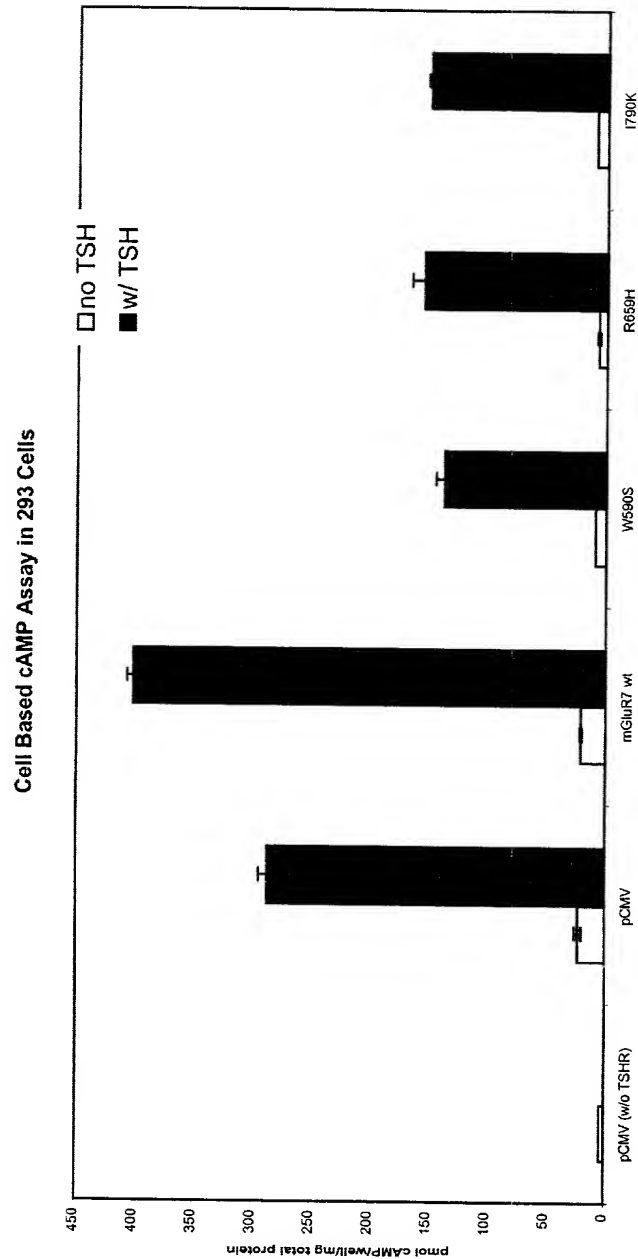


Figure 4



Co-Transfection with TSHR(A623I)

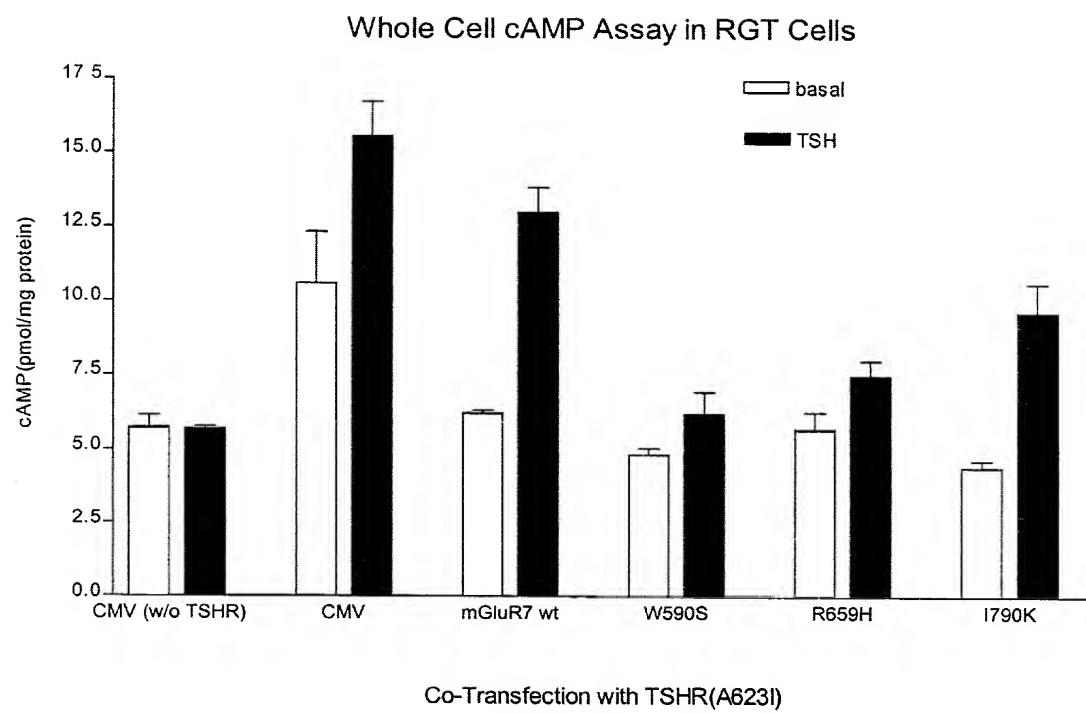


Figure 5

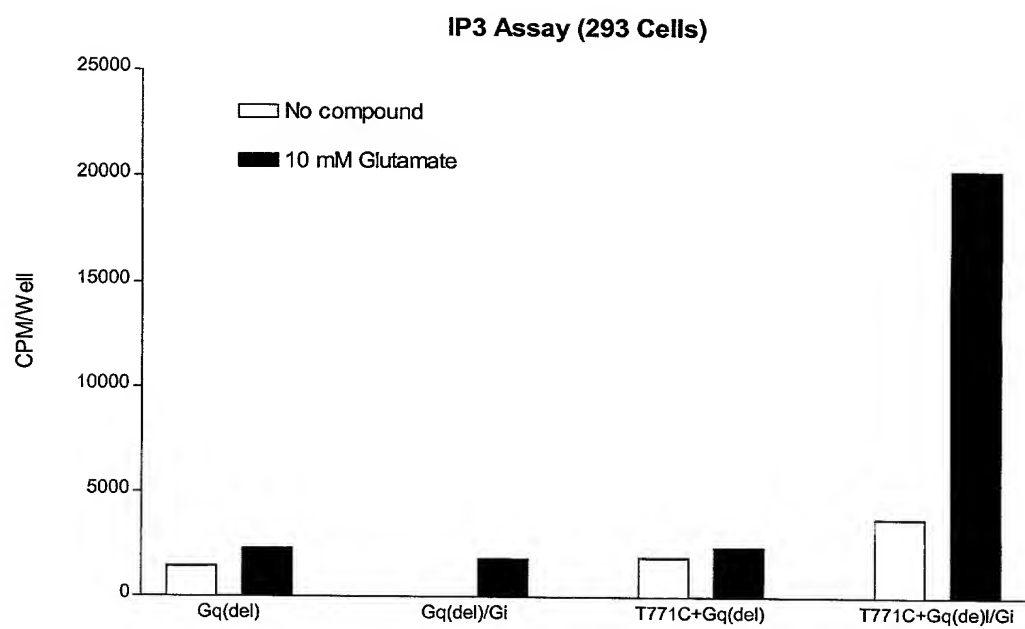


Figure 6

### SRE Reporter Assay

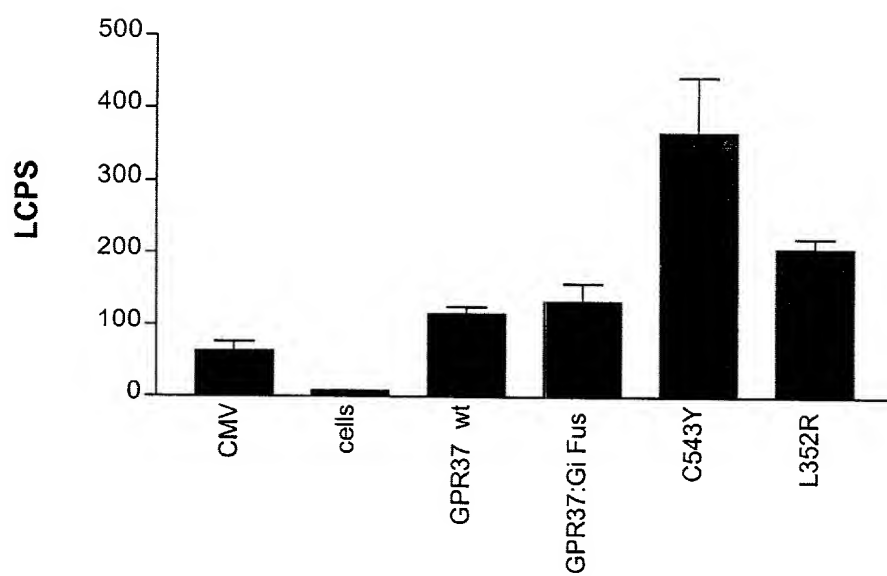
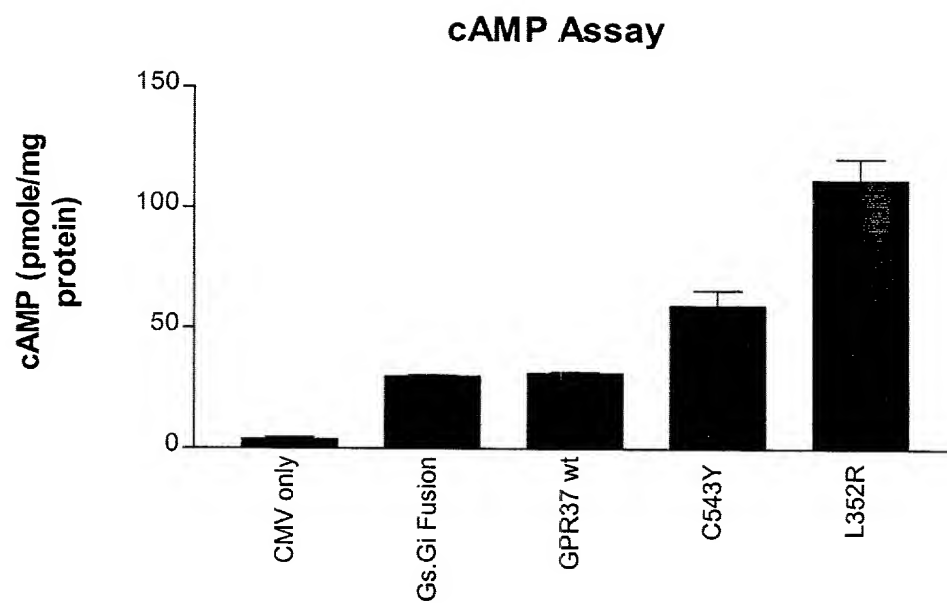


Figure 7



**Co-transfection with Gs/Gi Fusion**

**Figure 8**



# Northern Analysis of GPCR GPR37 expression in forskolin treated Rat Schwann cells

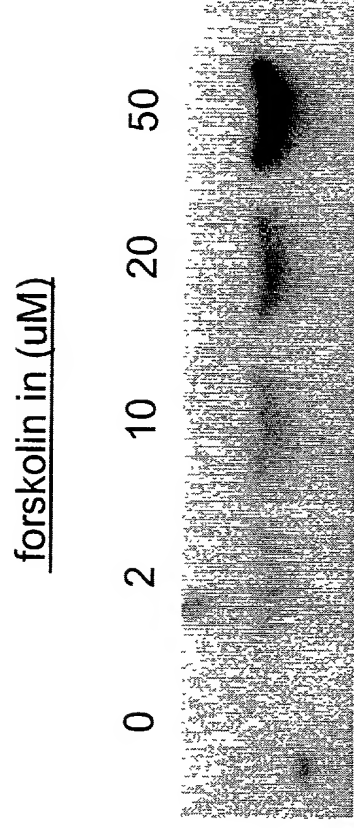


Figure 9

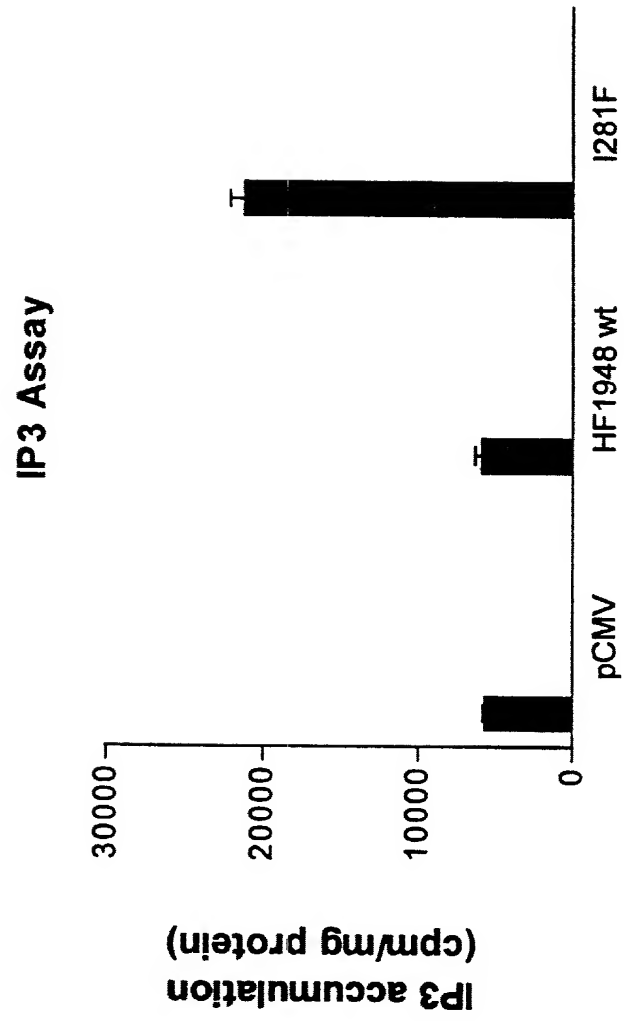
# Northern Analysis of GPCR GPR37 Expression in Crushed Rat Sciatic Nerve

Days post-crush

0      1      3      7      10      13



Figure 10



**Figure 11**

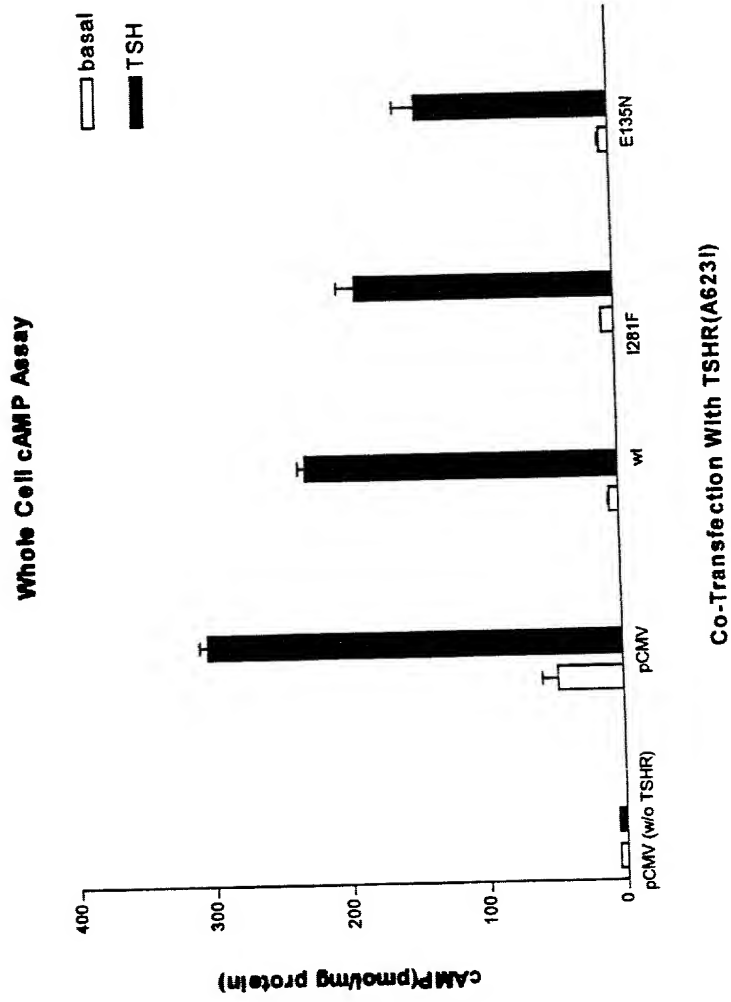
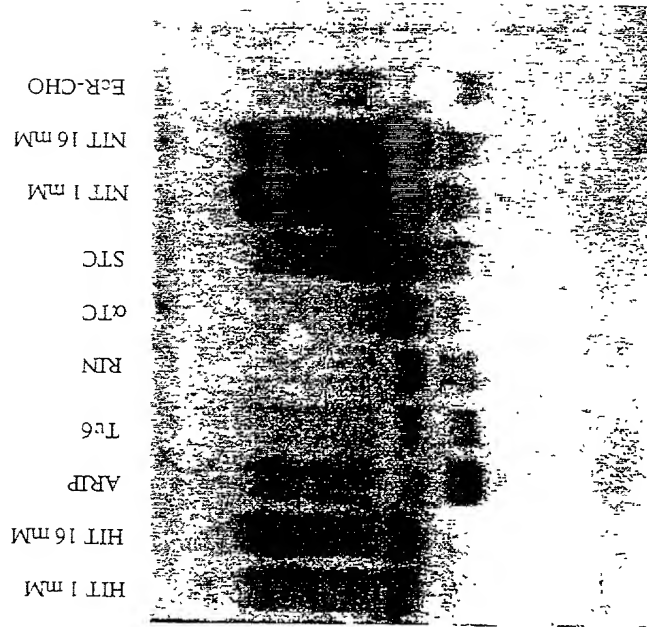


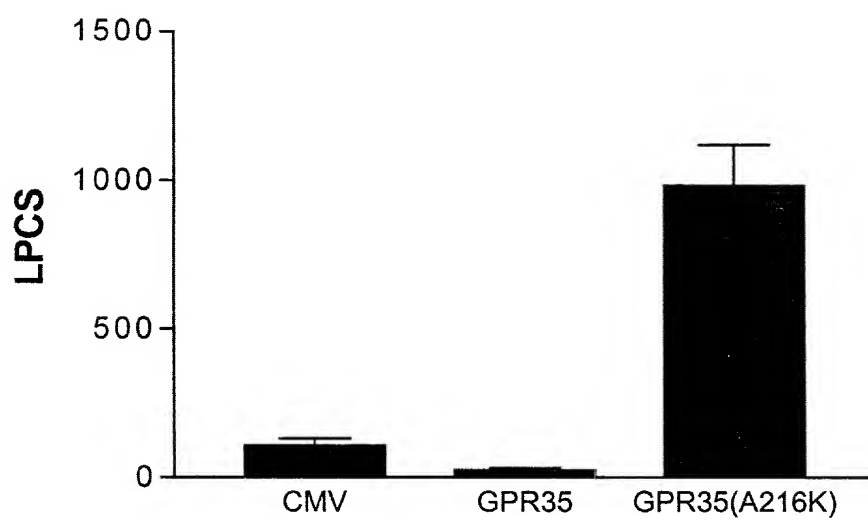
Figure 12

Figure 13

# Cell-specific expression of GPR66 variants in pancreatic cell lines



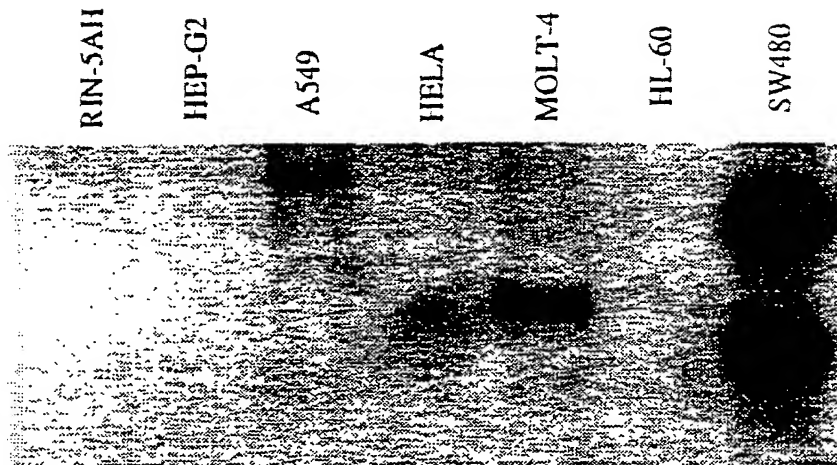
**E2F-Luc activation by GPR35 in  
293A cells**



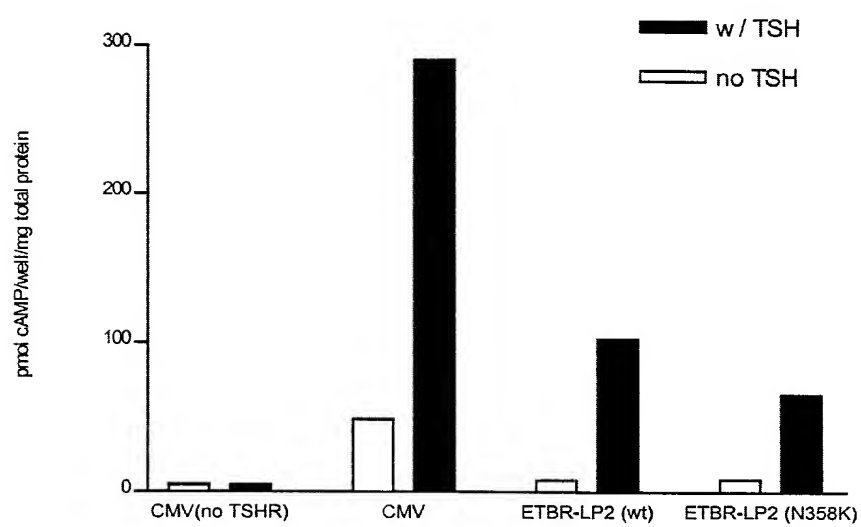
**Figure 14**

Figure 15

**Expression of GPR35  
in colorectal cancer cells**



### Adenylate Cyclase Assay



Co-Transfection with TSHR(A623I)

Figure 16



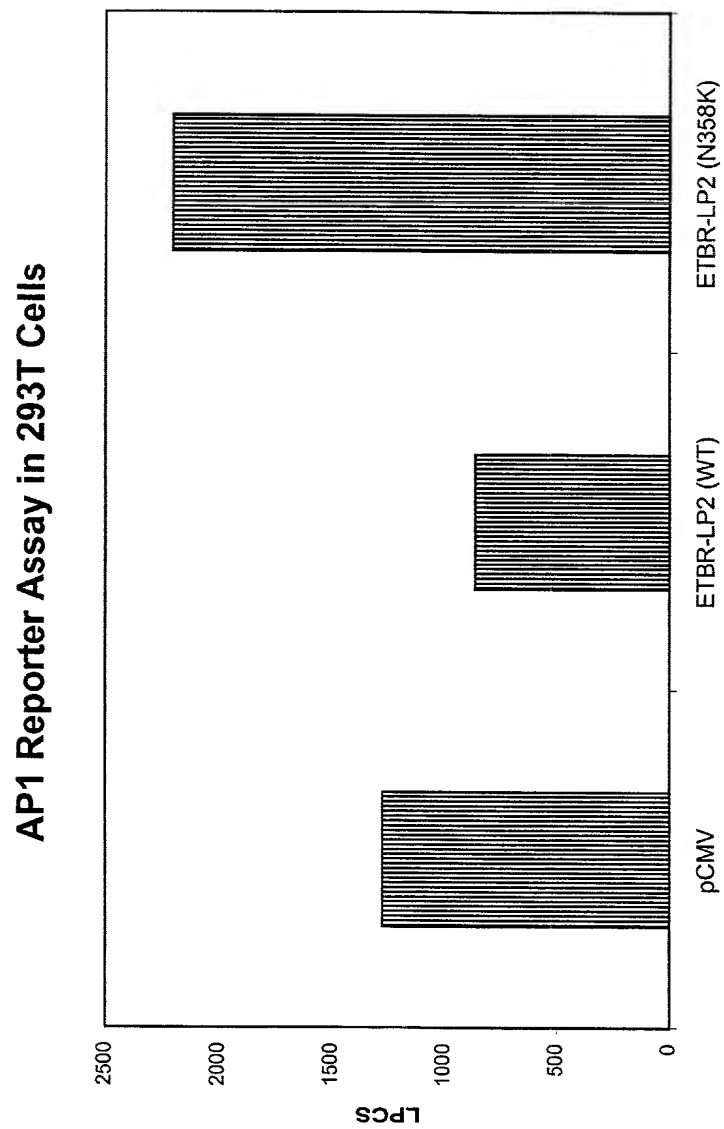


Figure 17

# **Northern Analysis of ETBR-LP2 in Forskolin Treated Rat Schwann Cells**

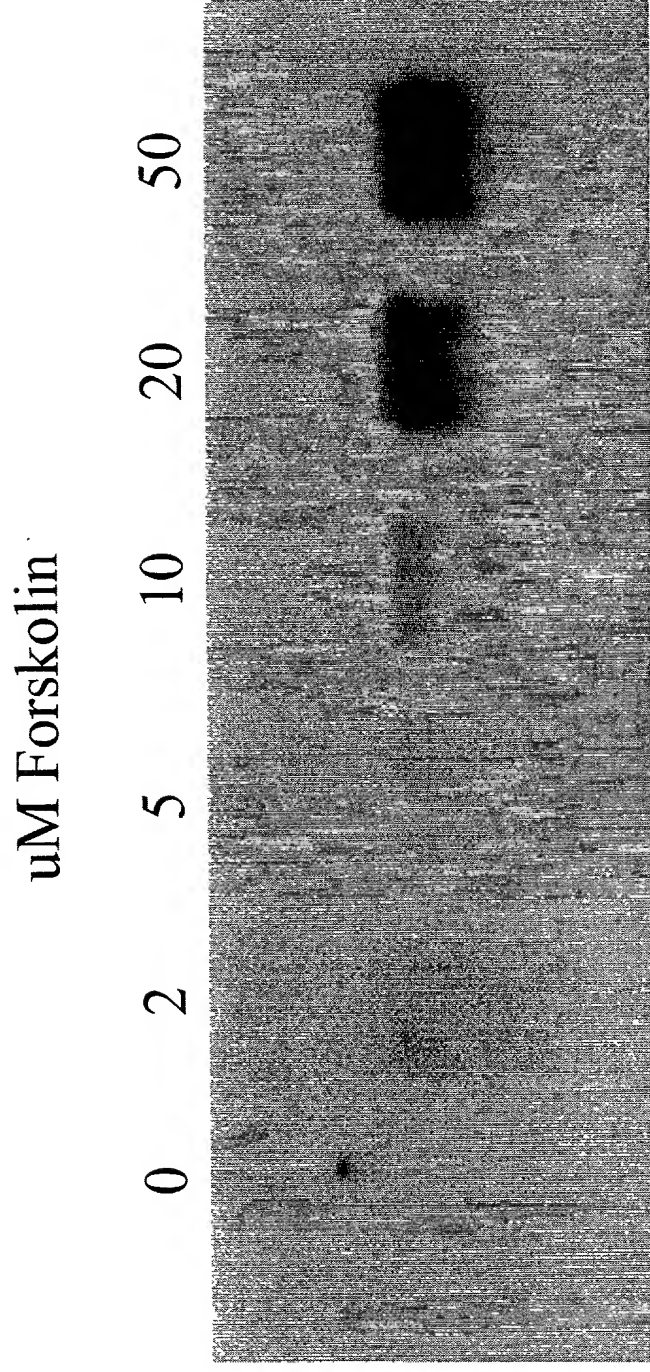


Figure 18

# Northern Analysis of ETBR-LP2 Expression in Crushed Rat Sciatic Nerve

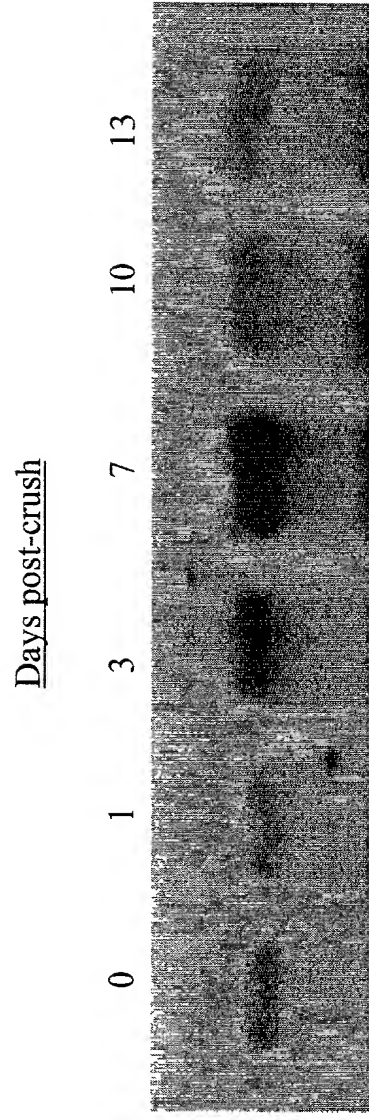


Figure 19

Figure 20A

	M R A L G A L A A S L A V L L A V G L L K V S G G A A L G V G P A S R N E T C L	Majority
	10 20 30 40	
1	M R W L W P L A V S L A V I L A V G L S R V S G G A P L H L G - - - - -	HETERLP2p
1	M R A P G A L L A R M S R L L L L L L L K V S A S S A L G V A P A S R N E T C L	HGPR37p
	G E S C A P T V I Q R R G R D A W G P G N S A R D V L R A R A E T E E Q G A A F	Majority
	50 60 70 80	
32	- - - - - R H R A E T Q E Q Q S - -	HETERLP2p
41	G E S C A P T V I Q R R G R D A W G P G N S A R D V L R A R A P R E E Q G A A F	HGPR37p
	L A G P S W D L P A A P G R D P A A G R G A E A S A A G P P G P P T R P P G P W	Majority
	90 100 110 120	
43	- - - - -	HETERLP2p
81	L A G P S W D L P A A P G R D P A A G R G A E A S A A G P P G P P T R P P G P W	HGPR37p
	R W K G A R G T E P S E T L G R G N P T A L Q L F L Q I S D E E A K G V Q G A G	Majority
	130 140 150 160	
43	- - R S K R G T E - - - - - D E E A K G V Q - - -	HETERLP2p
121	R W K G A R G Q E P S E T L G R G N P T A L Q L F L Q I S E E E E K G P R G A G	HGPR37p
	I S G R S Q E Q S V Q T V P G A S A L F Y R P I H A G G L Q G S H H K P L V A T	Majority
	170 180 190 200	
58	- - - - - Q Y V P E E W A E Y P R P I H P A G L Q P T - - K P L V A T	HETERLP2p
161	I S G R S Q E Q S V K T V P G A S D L F Y W P R R A G K L O G S H H K P L S K T	HGPR37p
	A N G L A G D G G W T I A L P G S G L A L N G S L G G G I H E P G G P R R G N S	Majority
	210 220 230 240	
86	S P N P D K D G G - - - - T P D S G Q E L R G N L T G A - - - P G - - - - -	HETERLP2p
201	A N G L A G H E G W T I A L P G R A L A Q N G S L G E G I H E P G G P R R G N S	HGPR37p
	T N Q R V Q L Q N P L Y P V T E S S Y G A Y A V M L L A V V V F G V G I V G N L	Majority
	250 260 270 280	
112	- - Q R L Q I Q N P L Y P V T E S S Y S A Y A I M L L A L V V F A V G I V G N L	HETERLP2p
241	T N R R V R L K N P F Y P L T Q E S Y G A Y A V M C L S V V I F G T G I I G N L	HGPR37p
	A V M C I V W H S Y Y L K S A S N S L L A S L A L W D F L V L F F C L P L V I F	Majority
	290 300 310 320	
150	S V M C I V W H S Y Y L K S A W N S I L A S L A L W D F L V L F F C L P I V I F	HETERLP2p
281	A V M C I V C H N Y Y M R S I S N S L L A N L A F W D F L I I F F C L P L V I F	HGPR37p
	N E L T K Q R L L G D V S C K A V P F I E V A S L G V T T F S L C A L G I D R F	Majority
	330 340 350 360	
190	N E I T K O R L L G D V S C R A V P F M E V S S L G V T T F S L C A L G I D R F	HETERLP2p
321	H E L T K K W L L E D F S C K I V P Y I E V A S L G V T T F T L C A L C I D R F	HGPR37p

Figure 20B

	HAATSVLMKVEMIENCSSILAKLAVIWVGALLLAVPEVVL	Majority
	370 380 390 400	
230	HVATSTLPKVRPIERCQSILAKLAVIWVGSMTLAVPELL	HETERLP2p
361	RAATNVQMYEEMIENCSSTTAKLAVIWVGALLLALPEVVL	HGPR37p
	RQLAQEDAGFSGRGTADSCIISKISASLPDSLVLALTYDS	Majority
	410 420 430 440	
270	WQLAQEPAA--PTMGTLDSCLMKPSASLPESLYSLVMTYQN	HETERLP2p
401	ROLSKEDLGFSGRAPAEERCIISKISPDLPDTIYVLALTYDS	HGPR37p
	ARLWWYFGCYFCLPILFTVTCSLVTARKVIRGAPGRESACT	Majority
	450 460 470 480	
308	ARMWWYFGCYFCLPILFTVTCLVLT-WRVIRGPGRKSECT-	HETERLP2p
441	ARLWWYFGCYFCLPILFTVTITCSLVTARKIRKA---EKACT	HGPR37p
	RGSKHEIQLESQNLNSTVVGTLTVVYGFCILPENVCNIVVAY	Majority
	490 500 510 520	
346	RASKHE-QCESQNLNSTVVGTLTVVYAFCTLPENVCNIVVAY	HETERLP2p
478	RGNKRQIQLESQMNCTVVALTILYGFCTIPENICNIVTAY	HGPR37p
	LATGVSSQOTLDDLGLISQFLLFKGAIVPVLCLCKPLG	Majority
	530 540 550 560	
385	LSTELTRQTLDDLGLINQFSTFFKGAITPVLCLCICRPLG	HETERLP2p
518	MATGVSSQOTMDLLNIISQFLLFKSCVTPVLLFCLCKPFS	HGPR37p
	QAFLDCCCCCCEECGGASSAVAADGSDNELTTEVSLSIF	Majority
	570 580 590 600	
425	QAFLDCCCCCCEECGGASSEASAAANGSDNKLKTEVSSSIY	HETERLP2p
558	RAFMECCCCCCEECIQKSSSTVTSDDNDNEYTTELELSPF	HGPR37p
	STIRRESSTLASVGTHC	Majority
	610	
465	FHKPRESPPLLPLGTPC	HETERLP2p
597	STIRREMSTFASVGTHC	HGPR37p

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Decoration 'Decoration #2': Box residues that match the Consensus exactly.